

SEQUENCE LISTING

<110> Ozelius, Laurie J.
Breakefield, Xandra O.

<120> TORSIN, TORSIN-RELATED GENES, AND
METHODS OF DETECTING NEURONAL DISEASES

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<150> US 09/218,363
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<150> US 09/099,454
<151> 1998-06-18

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<151> 1997-06-19

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Met Lys Leu Gly Arg Ala Val Leu Gly
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Leu Leu Leu Leu Ala Pro Ser Val Val Gln Ala Val Glu Pro Ile Ser
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Ser Arg Val Ala Glu Glu Met Thr Phe Phe Pro Lys Glu Glu Arg Val	
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35 40 45
Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
50 55 60
Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
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Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
85 90 95

Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160
 Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175
 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
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 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
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 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
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 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
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 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
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Pro Ser Ala Ala Gly Glu Arg Pro Leu Asn Ala Ser Ala Leu Lys	
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Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser	
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Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln	
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Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg	
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Glu Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly	
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 Asn Asn Lys Asn Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp
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 Ala Gly Thr Gly Lys Asn Phe Val Ser Gln Ile Val Ala Glu Asn Leu
 65 70 75 80
 His Pro Lys Gly Leu Lys Ser Asn Phe Val His Leu Phe Val Ser Thr
 85 90 95
 Leu His Phe Pro His Glu Gln Lys Ile Lys Leu Tyr Gln Asp Gln Leu
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 Gln Lys Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Asn Ser Val Phe
 115 120 125
 Ile Phe Asp Glu Met Asp Lys Leu His Pro Gly Ile Ile Asp Ala Ile
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 Lys Pro Phe Leu Asp Tyr Tyr Glu Gln Val Asp Gly Val Ser Tyr Arg
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 Lys Ala Ile Phe Ile Phe Leu Ser Asn Ala Gly Gly Asp Leu Ile Thr
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 Lys Thr Ala Leu Asp Phe Trp Arg Ala Gly Arg Lys Arg Glu Asp Ile
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 Gln Leu Lys Asp Leu Glu Pro Val Leu Ser Val Gly Val Phe Asn Asn
 195 200 205
 Lys His Ser Gly Leu Trp His Ser Gly Leu Ile Asp Lys Asn Leu Ile
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 Asp Tyr Phe Ile Pro Phe Leu Pro Leu Glu Tyr Arg His Val Lys Met
 225 230 235 240
 Cys Val Arg Ala Glu Met Arg Ala Arg Gly Ser Ala Ile Asp Glu Asp
 245 250 255
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aaa gag gag aga gtt ttc tca gat aaa ggc tgc aaa acg gtg ttc acc Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr 310 315 320	1014
aag tta gat tat tac tac gat gat tgacagtcat gattggcagc cgaggactact Lys Leu Asp Tyr Tyr Asp Asp 325 330	1068
gcctggagtt ggaaaagaaa caacactcag tccttccaca cttccacccc cagctccccc ccctgaaaga ggaatccagt gaatgttccct gtttgatgtg acaggaattc tccctggcat tgtttccacc ccctgggtgcc tgcaggccac ccagggacca cggcgagga cgtgaaggct cccgaaacacg cacagaagga aggagccagc tcccgccca ctcatcgccag ggctcatgat tttttacaaa ttatgttttta attccaagtgt tttctgtttc aaggaaggat gaataagtt tattaaaaat gtggtaactt tattaaaaat gatTTTaaC attatgagag actgctcaga ttctaagttt tgcccttgg tgggtgttt ttTTTaaGt tctcatcatt attacataga ctgtgaagta ctTTTactgg aaatgagccc aagcacacat gcatggcatt tgTTTCTGAA caggagggca tccctggggta tgggtgtgg acatgagcca gctctgtccc aggatggtcc cagcggatgc tgccaggggc agtgaagtgt ttaggtgaag gacaagttagg taagaggacg ccttcaggca ccacagataa gcctgaaaca gcctctccaa gggTTTcAC cttAGcaaca atgggagctg tgggagtgat ttggccaca ctgtcaacat ttgttagaac cagtcttttgc aaagaaaaagt atttccaact tgcacttgc cagtcaactcc gttttgcaaa aggtggccct tcactgtcca ttccaaatag cccacacgtg ctctctgctg gattctaaat tatgtgaatt ttgccccatatt aaatcttccct cattatactt attatTTGTT acgttcaatc agaatccccg aaacccctcta taaagcttag ctgcccccttc tgaggatgt gagaacggtg tctttcttta taaatgcAAA tggctaccgt ttacaataa aattttgcat gtgc	1128 1188 1248 1308 1368 1428 1488 1548 1608 1668 1728 1788 1848 1908 1968 2028 2072

<210> 6
<211> 332
<212> PRT
<213> Homo sapien

<400> 6	
Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser	
1 5 10 15	
Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly	
20 25 30	
Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu	
35 40 45	
Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp	
50 55 60	
Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu	
65 70 75 80	
Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu	
85 90 95	
Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser	
100 105 110	
Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr	
115 120 125	
Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile	
130 135 140	
Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser	
145 150 155 160	

Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175
 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190
 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205
 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220
 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270
 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300
 Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
 305 310 315 320
 Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
 325 330

<210> 7
 <211> 2504
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (2)...(799)

<400> 7
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 Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val Ile
 1 5 10 15

 ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa cca 97
 Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys Pro
 20 25 30

 ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt gtc 145
 Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe Val
 35 40 45

 agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt aac 193
 Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser Asn
 50 55 60

 ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag aag 241
 Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln Lys
 65 70 75 80

 ata aaa ctg tac cag gac cag tta cag aag tgg atc cgc ggt aat gtg 289
 Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn Val
 85 90 95

agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa ttg	337
Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys Leu	
100 105 110	
cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac gag	385
His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu	
115 120 125	
cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc agc	433
Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser	
130 135 140	
aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cgg	481
Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg	
145 150 155 160	
gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta	529
Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val	
165 170 175	
ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	577
Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser	
180 185 190	
gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	625
Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro	
195 200 205	
ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673
Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala	
210 215 220	
cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721
Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu	
225 230 235 240	
atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769
Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys	
245 250 255	
aag act gtg cag tcg cgg ctg gat ttc cac tgagctccata tccagatggg	819
Lys Thr Val Gln Ser Arg Leu Asp Phe His	
260 265	
gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879
gaccgcgttg gggtttgcg tgtttgcacc ttagactttt gggtatagaa tctttttttt	939
gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactca	999
gcaacctccg ctccccggttt gagtgattct catgcctcag cctcccgggt agctgggatt	1059
acaggcatga gcccactgtgc ccagctggga tatagaatct aagagtttatgttggaaaac	1119
acgtgaatctt attgcgcgca tttgtcattt agcaagatgg cagcagtccca gttgttcttt	1179
gcagctggag atgaactttt aaaaatcccc ttcacactta atgtactgac cgagacagaa	1239
gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccac cagcacccgc	1299
gcctcagaag ctacggcgtcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359
ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419
tttgcctgtt ctcgttctttt acacagagtt cactgactt aagtataactc agttaaaatc	1479
ggggctggag gtgcagacgg tgcgttgcaccg gaggatgtgg ccgtgcggc cgagactct	1539
tgtatctgacg tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599
gcagcagacc tggacagacaa ggccctccccc gcctgtccat cgctctagct gctaatacag	1659
ccctggctgtt ggaatccttc accgtctcag ctggtatcag ccccaaccat cttgggtgcc	1719
atatctcagc ttggatctct gctagagtcc ccccaaccat atatcataga gttgaatcac	1779

aatgagaccg ttggcttga atttgagtcg ttggttccca tggtagatg cttgttaaga 1839
 ctttatactt gggtaatct ctcacttat tttgtagaac cattgaaat cctaggatgt 1899
 gcttgttctg gaaggatgac atggcccaag actgaacaag tcagcttgc gatcttaat 1959
 gatggaaagta taggacgtt cttatTTAA aacaaggggaa ggacacaaaa tggaatgact 2019
 gccttagtcc tttctcagat actcctaaa acaattttt attgtttaaa tttgtggtaa 2079
 tacatggtca caaccgtgga tcaaacaagg tcagtctaaa gtggcaggc ctaggtgtga 2139
 cctgatacca ccacccttg tggcagcacc gggctggact gccctgatcc ctgggacgtg 2199
 agacttagct tccagccagt gtgaatcatt gtatctgtct cataatcaca gcacagctgc 2259
 agacacaaca acgtgcagca tttttacat aaaaatatgg tagaattaat ttatgacatg 2319
 gaaatgcctt acgtggatc acacttagtc ttgaaaaaaaaa caccagggtg acgtttaaaa 2379
 ttttagtac atatcctcaa attggagcta agttatactt ctttataac cttttggca 2439
 tctggtcgag agaagacaag attttctcta ttacagtga ggcaataaat atgtttgcc 2499
 cctt 2504

<210> 8

<211> 266

<212> PRT

<213> Homo sapien

<400> 8

Asp	Leu	Glu	Glu	Lys	Leu	Phe	Gly	Gln	His	Leu	Ala	Thr	Glu	Val	Ile
1	.	5			10								15		
Phe	Lys	Ala	Leu	Thr	Gly	Phe	Arg	Asn	Asn	Lys	Asn	Pro	Lys	Lys	Pro
				20				25					30		
Leu	Thr	Leu	Ser	Leu	His	Gly	Trp	Ala	Gly	Thr	Gly	Lys	Asn	Phe	Val
				35				40				45			
Ser	Gln	Ile	Val	Ala	Glu	Asn	Leu	His	Pro	Lys	Gly	Leu	Lys	Ser	Asn
	50				55				60						
Phe	Val	His	Leu	Phe	Val	Ser	Thr	Leu	His	Phe	Pro	His	Glu	Gln	Lys
	65				70				75				80		
Ile	Lys	Leu	Tyr	Gln	Asp	Gln	Leu	Gln	Lys	Trp	Ile	Arg	Gly	Asn	Val
				85				90				95			
Ser	Ala	Cys	Ala	Asn	Ser	Val	Phe	Ile	Phe	Asp	Glu	Met	Asp	Lys	Leu
	100					105				110					
His	Pro	Gly	Ile	Ile	Asp	Ala	Ile	Lys	Pro	Phe	Leu	Asp	Tyr	Tyr	Glu
	115					120				125					
Gln	Val	Asp	Gly	Val	Ser	Tyr	Arg	Lys	Ala	Ile	Phe	Ile	Phe	Leu	Ser
	130				135				140						
Asn	Ala	Gly	Gly	Asp	Leu	Ile	Thr	Lys	Thr	Ala	Leu	Asp	Phe	Trp	Arg
	145				150				155				160		
Ala	Gly	Arg	Lys	Arg	Glu	Asp	Ile	Gln	Leu	Lys	Asp	Leu	Glu	Pro	Val
					165			170				175			
Leu	Ser	Val	Gly	Val	Phe	Asn	Asn	Lys	His	Ser	Gly	Leu	Trp	His	Ser
				180			185				190				
Gly	Leu	Ile	Asp	Lys	Asn	Leu	Ile	Asp	Tyr	Phe	Ile	Pro	Phe	Leu	Pro
	195					200				205					
Leu	Glu	Tyr	Arg	His	Val	Lys	Met	Cys	Val	Arg	Ala	Glu	Met	Arg	Ala
	210					215				220					
Arg	Gly	Ser	Ala	Ile	Asp	Glu	Asp	Ile	Val	Thr	Arg	Val	Ala	Glu	Glu
	225					230				235				240	
Met	Thr	Phe	Phe	Pro	Arg	Asp	Glu	Lys	Ile	Tyr	Ser	Asp	Lys	Gly	Cys
					245			250				255			
Lys	Thr	Val	Gln	Ser	Arg	Leu	Asp	Phe	His						
			260			265									

<210> 9

<211> 332

<212> PRT

<213> Homo sapien

<400> 9
 Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Ala Pro Ser
 1 5 10 15
 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
 20 25 30
 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
 35 40 45
 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95
 Thr Leu Ser Leu His Gly Trp Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160
 Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175
 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190
 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205
 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220
 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270
 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300
 Thr Phe Phe Pro Lys Glu Glu Pro Val Phe Ser Asp Lys Gly Cys Lys
 305 310 315 320
 Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
 325 330

<210> 10
<211> 267
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (1)...(267)
<223> Xaa = any amino acid

<400> 10
 Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val
 1 5 10 15
 Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys
 20 25 30

Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe
 35 40 45
 Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser
 50 55 60
 Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln
 65 70 75 80
 Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn
 85 90 95
 Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys
 100 105 110
 Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr
 115 120 125
 Glu Gln Val Asp Gly Val Ser Tyr Xaa Lys Ala Ile Phe Ile Phe Leu
 130 135 140
 Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp
 145 150 155 160
 Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro
 165 170 175
 Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His
 180 185 190
 Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu
 195 200 205
 Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg
 210 215 220
 Ala Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu
 225 230 235 240
 Glu Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gln
 245 250 255
 Cys Lys Thr Val Gln Ser Arg Leu Asp Phe His
 260 265

<210> 11
 <211> 334
 <212> PRT
 <213> C. elegans

<400> 11

Met Trp Met Lys Leu Asp Tyr Val Leu Leu Leu Phe His Leu Cys
 1 5 10 15
 Phe Val Asn Thr Glu Leu Ile Ser Val Ile Thr Gly Lys Ile Lys Asp
 20 25 30
 Ser Gly Thr Thr Ile Ala Ile Ser Ala Gly Ala Phe Trp Gly Leu Lys
 35 40 45
 Asp Arg Leu Lys Cys Tyr Leu Tyr Glu Cys Cys His Glu Pro Asp Val
 50 55 60
 Asn Phe Asn Tyr His Thr Leu Asp Ala Asp Ile Ala Asn Leu Leu Phe
 65 70 75 80
 Gly Gln His Leu Val Lys Asp Val Val Val Asn Ser Ile Lys Ser His
 85 90 95
 Trp Tyr Asn Glu Asn Pro Arg Lys Pro Leu Val Leu Ser Phe His Gly
 100 105 110
 Tyr Thr Gly Ser Gly Lys Asn Tyr Val Ala Glu Ile Ile Ala Asn Asn
 115 120 125

Thr Phe Arg Leu Gly Leu Arg Ser Thr Phe Val Gln His Ile Val Ala
 130 135 140
 Thr Asn Asp Phe Pro Asp Lys Asn Lys Leu Glu Glu Tyr Gln Val Glu
 145 150 155 160

Leu Arg Asn Arg Ile Leu Thr Thr Val Gln Lys Cys Gln Arg Ser Ile
 165 170 175
 Phe Ile Phe Asp Glu Ala Asp Lys Leu Pro Glu Gln Leu Leu Gly Ala
 180 185 190
 Ile Lys Pro Phe Leu Asp Tyr Tyr Ser Thr Ile Ser Gly Val Asp Phe
 195 200 205
 Arg Arg Ser Ile Phe Ile Leu Leu Ser Asn Lys Gly Gly Gly Glu Ile
 210 215 220
 Ala Arg Ile Thr Lys Glu Gln Tyr Glu Ser Gly Tyr Pro Arg Glu Gln
 225 230 235 240
 Leu Arg Leu Glu Ala Phe Glu Arg Glu Leu Met Asn Phe Ser Tyr Asn
 245 250 255
 Glu Lys Gly Leu Gln Met Ser Glu Leu Ile Ser Asn His Leu Ile
 260 265 270
 Asp His Phe Val Pro Phe Leu Pro Leu Gln Arg Glu His Val Arg Ser
 275 280 285
 Cys Val Gly Ala Tyr Leu Arg Lys Arg Gly Arg Gly Asp Leu Val Ser
 290 295 300
 Asn Val Asp Phe Val Glu Arg Val Leu Asn Ser Leu Gln Tyr Phe Pro
 305 310 315 320
 Glu Ser Ser Lys Ala Phe Ser Ser Ser Gly Cys Lys Arg Val
 325 330

<210> 12
 <211> 268
 <212> PRT
 <213> Homo sapien

<400> 12

Leu Glu Cys Asp Leu Ala Gln His Leu Ala Gly Gln His Leu Ala Lys
 1 5 10 15
 Ala Leu Val Val Lys Ser Leu Lys Ala Phe Val Gln Asp Pro Ala Pro
 20 25 30
 Ser Lys Pro Leu Val Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys
 35 40 45
 Ser Tyr Val Ser Ser Leu Leu Ala Gln His Leu Phe Arg Asp Gly Leu
 50 55 60
 Arg Ser Pro His Val His His Phe Ser Pro Ile Ile His Phe Pro His
 65 70 75 80
 Pro Ser Arg Thr Glu Gln Tyr Lys Lys Glu Leu Lys Ser Trp Val Gln
 85 90 95
 Gly Asn Thr Ala Cys Glu Arg Ser Leu Phe Leu Phe Asp Glu Met Asp
 100 105 110
 Lys Leu Pro Pro Gly Leu Met Glu Val Leu Gln Pro Phe Leu Gly Pro
 115 120 125
 Ser Trp Val Val Tyr Gly Thr Asn Tyr Arg Lys Ala Ile Phe Ile Phe
 130 135 140
 Ile Ser Asn Ala Gly Gly Glu Cys Ile Asn Gln Val Ala Leu Glu Ala
 145 150 155 160
 Trp Arg Thr Asn Arg Asp Arg Glu Glu Ile Ser Leu Gln Glu Val Glu
 165 170 175
 Pro Val Ile Ser Arg Ala Val Met Asp Asn Pro Gln His Gly Phe Trp
 180 185 190
 Arg Ser Gly Ile Met Glu Glu His Leu Leu Asp Ala Val Val Pro Phe
 195 200 205
 Leu Pro Leu Gln Arg His His Val Arg His Cys Val Leu Asn Glu Leu
 210 215 220
 Ala Gln Leu Gly Leu Glu Pro Ala Arg Arg Trp Phe Arg Arg Cys Trp
 225 230 235 240

Thr Asp Thr Tyr Phe Pro Glu Val Glu Gln Leu Phe Ser Ser Asn Gly
 245 250 255
 Cys Lys Thr Val Ala Ser Arg Leu Thr Phe Phe Leu
 260 265

<210> 13
 <211> 177
 <212> PRT
 <213> Murine

<220>
 <221> VARIANT
 <222> (1)...(177)
 <223> Xaa = Any Amino Acid

<400> 13
 Ala Ala Ala Leu His Gln Thr Leu Phe Ile Phe Asp Glu Ala Glu Lys
 1 5 10 15
 Leu His Pro Gly Leu Leu Glu Val Leu Gly Pro His Leu Glu Arg Arg
 20 25 30
 Ala Pro Glu Xaa Xaa Gly Leu Ser Leu Xaa Trp Thr Ile Phe Leu Phe
 35 40 45
 Leu Ser Asn Leu Arg Gly Asp Ile Ile Asn Glu Val Val Leu Lys Leu
 50 55 60
 Leu Lys Ala Gly Trp Ser Arg Glu Glu Ile Thr Met Glu His Leu Glu
 65 70 75 80
 Pro His Leu Gln Ala Glu Ile Val Asp Asp His Arg Gln Trp Leu Trp
 85 90 95
 His Ser Arg Leu Val Lys Glu Asn Leu Ile Asp Tyr Phe Ile Pro Phe
 100 105 110
 Leu Pro Leu Glu Tyr Arg His Val Arg Leu Cys Ala Arg Asp Ala Phe
 115 120 125
 Leu Ser Gln Glu Leu Leu Tyr Lys Glu Glu Thr Leu Asp Glu Ile Ala
 130 135 140
 Gln Met Met Val Tyr Val Pro Lys Glu Glu Gln Leu Phe Ser Ser Gln
 145 150 155 160
 Gly Cys Lys Ser Ile Xaa Gln Arg Ile Lys Leu Leu Pro Val Met Xaa
 165 170 175
 Gly

<210> 14
 <211> 214
 <212> PRT
 <213> Murine

<400> 14
 Glu Glu His Pro Leu Val Phe Leu Phe Leu Gly Ser Ser Gly Ile Gly
 1 5 10 15
 Lys Thr Glu Leu Ala Lys Gln Thr Ala Lys Tyr Met His Lys Asp Ala
 20 25 30
 Lys Lys Gly Phe Ile Arg Leu Asp Met Ser Glu Phe Gln Glu Arg His
 35 40 45
 Glu Val Ala Lys Phe Ile Gly Ser Pro Arg Gly Tyr Ile Gly His Glu
 50 55 60
 Glu Gly Gly Gln Leu Thr Lys Lys Leu Lys Gln Cys Pro Asn Ala Val
 65 70 75 80

Val Leu Phe Asp Glu Val Asp Lys Ala His Pro Asp Val Leu Thr Ile
 85 90 95
 Met Leu Gln Leu Phe Asp Glu Gly Arg Leu Thr Asp Gly Lys Gly Lys
 100 105 110
 Thr Ile Asp Cys Lys Asp Ala Ile Phe Ile Met Thr Ser Asn Val Ala
 115 120 125
 Ser Asp Glu Ile Ala Gln His Ala Leu Gln Leu Arg Gln Glu Ala Leu
 130 135 140
 Glu Met Ser Arg Asn Arg Ile Ala Glu Asn Leu Gly Asp Val Gln Met
 145 150 155 160
 Ser Asp Lys Ile Thr Ile Ser Lys Asn Phe Lys Glu Asn Val Ile Arg
 165 170 175
 Pro Ile Leu Lys Ala His Phe Arg Arg Asp Glu Phe Leu Gly Arg Ile
 180 185 190
 Asn Glu Ile Val Tyr Phe Leu Pro Phe Cys His Ser Glu Leu Ile Gln
 195 200 205
 Leu Val Asn Lys Glu Leu
 210

<210> 15
 <211> 185
 <212> PRT
 <213> Unknown

<220>
 <223> Soybean

<400> 15
 Pro Gln Gln Pro Thr Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val
 1 5 10 15
 Gly Lys Thr Glu Leu Ala Lys Ala Leu Ala Glu Gln Leu Phe Asp Asn
 20 25 30
 Glu Asn Gln Leu Val Arg Ile Asp Met Ser Glu Tyr Met Glu Gln His
 35 40 45
 Ser Val Ser Arg Leu Ile Gly Ala Pro Pro Gly Tyr Val Gly His Glu
 50 55 60
 Glu Gly Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Ser Val
 65 70 75 80
 Val Leu Phe Asp Glu Val Glu Lys Ala His Thr Ser Val Phe Asn Ile
 85 90 95
 Leu Leu Gln Val Leu Asp Asp Gly Arg Leu Thr Asp Gly Gln Gly Arg
 100 105 110
 Thr Val Asp Phe Arg Asn Thr Val Ile Ile Met Thr Ser Asn Leu Gly
 115 120 125
 Ala Glu His Leu Leu Ser Gly Ser Gln Lys Cys Thr Met Gln Val Ala
 130 135 140
 Arg Asp Arg Val Met Glu Gln Glu Arg Arg Gln Phe Arg Pro Glu Leu
 145 150 155 160
 Leu Asn Arg Leu Asp Glu Ile Val Val Phe Asp Pro Leu Ser His Asp
 165 170 175
 Gln Leu Arg Lys Val Ala Arg Leu Met
 180 185

<210> 16
 <211> 194
 <212> PRT
 <213> Homo sapien

<400> 16

Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly
 1 5 10 15
 Lys Asn Phe Val Ser Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly
 20 25 30
 Leu Asn Ser Asp Tyr Val His Leu Phe Val Ala Thr Leu His Phe Pro
 35 40 45
 His Ala Ser Asn Ile Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile
 50 55 60
 Arg Gly Asn Val Ser Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu
 65 70 75 80
 Met Asp Lys Met His Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu
 85 90 95
 Asp Tyr Tyr Asp Leu Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe
 100 105 110
 Ile Phe Leu Ser Asn Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu
 115 120 125
 Asp Phe Trp Arg Ser Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp
 130 135 140
 Ile Glu His Ala Leu Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly
 145 150 155 160
 Phe Trp His Ser Ser Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val
 165 170 175
 Pro Phe Leu Pro Leu Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val
 180 185 190
 Glu Met

<210> 17
 <211> 194
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(194)
 <223> Xaa = Any Amino Acid

<400> 17
 Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly
 1 5 10 15
 Lys Asn Phe Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly
 20 25 30
 Leu Lys Ser Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro
 35 40 45
 His Glu Gln Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile
 50 55 60
 Arg Gly Asn Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu
 65 70 75 80
 Met Asp Lys Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu
 85 90 95
 Asp Tyr Tyr Glu Gln Val Asp Gly Val Ser Tyr Xaa Lys Ala Ile Phe
 100 105 110
 Ile Phe Leu Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu
 115 120 125
 Asp Phe Trp Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp
 130 135 140
 Leu Glu Pro Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly
 145 150 155 160

Leu Trp His Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile
 165 170 175
 Pro Phe Leu Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala
 180 185 190
 Glu Met

<210> 18
 <211> 192
 <212> PRT
 <213> C. elegans

<400> 18
 Pro Arg Lys Pro Leu Val Leu Ser Phe His Gly Tyr Thr Gly Ser Gly
 1 5 10 15
 Lys Asn Tyr Val Ala Glu Ile Ile Ala Asn Asn Thr Phe Arg Leu Gly
 20 25 30
 Leu Arg Ser Thr Phe Val Gln His Ile Val Ala Thr Asn Asp Phe Pro
 35 40 45
 Asp Lys Asn Lys Leu Glu Glu Tyr Gln Val Glu Leu Arg Asn Arg Ile
 50 55 60
 Leu Thr Thr Val Gln Lys Cys Arg Ser Ile Phe Ile Phe Asp Glu Ala
 65 70 75 80
 Asp Lys Leu Pro Glu Gln Leu Leu Gly Ala Ile Lys Pro Phe Leu Asp
 85 90 95
 Tyr Tyr Ser Thr Ile Ser Gly Val Asp Phe Arg Arg Ser Ile Phe Ile
 100 105 110
 Leu Leu Ser Asn Lys Gly Gly Glu Ile Ala Arg Ile Thr Lys Glu
 115 120 125
 Gln Tyr Glu Ser Gly Tyr Pro Arg Glu Gln Leu Arg Leu Glu Ala Phe
 130 135 140
 Glu Arg Glu Leu Met Asn Phe Ser Tyr Asn Glu Lys Gly Gly Leu Gln
 145 150 155 160
 Met Ser Glu Leu Ile Ser Asn His Leu Ile Asp His Phe Val Pro Phe
 165 170 175
 Leu Pro Leu Gln Arg Glu His Val Arg Ser Cys Val Gly Ala Tyr Leu
 180 185 190

<210> 19
 <211> 194
 <212> PRT
 <213> Homo sapien

<400> 19
 Pro Ser Lys Pro Leu Val Leu Ser Leu His Gly Trp Thr Gly Thr Gly
 1 5 10 15
 Lys Ser Tyr Val Ser Ser Leu Leu Ala Gln His Leu Phe Arg Asp Gly
 20 25 30
 Leu Arg Ser Pro His Val His His Phe Ser Pro Ile Ile His Phe Pro
 35 40 45
 His Pro Ser Arg Thr Glu Gln Tyr Lys Lys Glu Leu Lys Ser Trp Val
 50 55 60
 Gln Gly Asn Leu Thr Ala Cys Glu Arg Ser Leu Phe Leu Phe Asp Glu
 65 70 75 80
 Met Asp Lys Leu Pro Pro Gly Leu Met Glu Val Leu Gln Pro Phe Leu
 85 90 95
 Gly Pro Ser Trp Val Val Tyr Gly Thr Asn Tyr Arg Lys Ala Ile Phe
 100 105 110
 Ile Phe Ile Ser Asn Ala Gly Gly Glu Gln Ile Asn Gln Val Ala Leu
 115 120 125

<210> 20
<211> 128
<212> PRT
<213> Murine

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<220>
<221> VARIANT
<222> (1) ... (128)
<223> Xaa = Any Amino Acid
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<400> 20
Ala Ala Ala Leu His Gln Thr Leu Phe Ile Phe Asp Glu Ala Glu Lys
   1           5                   10                  15
Leu His Pro Gly Leu Leu Glu Val Leu Gly Pro His Leu Glu Arg Arg
   20          25                  30
Ala Pro Glu Xaa Xaa Gly Leu Ser Leu Xaa Trp Thr Ile Phe Leu Phe
   35          40                  45
Leu Ser Asn Leu Arg Gly Asp Ile Ile Asn Glu Val Val Leu Lys Leu
   50          55                  60
Leu Lys Ala Gly Trp Ser Arg Glu Glu Ile Thr Met Glu His Leu Glu
   65          70                  75                  80
Pro His Leu Gln Ala Glu Ile Val Asp Asp His Arg Gln Trp Leu Trp
   85          90                  95
His Ser Arg Leu Val Lys Glu Asn Leu Ile Asp Tyr Phe Ile Pro Phe
  100         105                 110
Leu Pro Leu Glu Tyr Arg His Val Arg Leu Cys Ala Arg Asp Ala Phe
  115         120                 125

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<210> 21  
<211> 253  
<212> DNA  
<213> Homo sapien
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<400> 21
cctggataac aaacacacctaa aatgtgttat ccgagtgaa atgcagtccc gaggctatga 60
aattgtatcaa gacattgtaa gcagagttgc tgaggagatg acattttcc ccaaagagga 120
gagagtttc tcagataaaag gctgcaaaaac ggtgttccacc aagtttagatt attactacga 180
tgattgacag tcatgattgg cagccggagt cactgcctgg agttggaaag aaacaacact 240
cagtcctcc acc                                         253
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<210> 22
<211> 253
<212> DNA
<213> *Homo sapien*

<400> 22
ggaccttatg tttgtggatt tttacacata qqctcacctt tacatcaggq tccgataactt 60

taactacttc tgtaacattc gtctcaccga ctcccttact gtaaaaaggg gtttctcctc 120
 tctcaaaaga gtctatttcc gacgtttgc caccaagtgg ttcaatctaa taatgatgct 180
 actaactgtc agtactaacc gtcggcctca gtgacggacc tcaaccttcc tttgttgtga 240
 gtcaggaagg tgg 253

<210> 23
 <211> 7
 <212> PRT
 <213> Homo sapien

<400> 23
 Phe Phe Thr Met Glu Ala Val
 1 5

<210> 24
 <211> 21
 <212> DNA
 <213> Homo sapien

<400> 24
 gtggctgaga tgacatTTT c 21

<210> 25
 <211> 24
 <212> DNA
 <213> Homo sapien

<400> 25
 gtggctgagg agatgacatt ttTC 24

<210> 26
 <211> 8
 <212> PRT
 <213> Homo sapien

<400> 26
 Phe Phe Thr Met Glu Glu Ala Val
 1 5

<210> 27
 <211> 205
 <212> DNA
 <213> Synthetic

<400> 27
 cctggataac aaacaccta aaatgtgtat ccgagtgaa atgcagtccc gaggctatga 60
 aattgtgaa gacattgtaa gcagagtggc tgaggagatg acatTTTCC ccaaagagga 120
 gagagTTTC tcagataaaag gctgaaaac ggtgttcacc aagtttagatt attactacga 180
 tgattgacag tcatgattgg cagcc 205

<210> 28
 <211> 19
 <212> DNA
 <213> Synthetic

<400> 28
 cctggataac aaacaccta 19

<210> 29

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<211> 20
<212> DNA
<213> Synthetic

<400> 29
ggctgccaat catgactgtc 20

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 30
gcaaaaacagg gctttgtacc g 21

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 31
agtagagacg cgggttagatg 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 32
gcgtctctac tgcctttcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 33
atgccctggc cctagttcag 20

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 34

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ggtttcgcaa ggtgcttggaa	20
<210> 35	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 35	
gggattccaa acttccatcc	20
<210> 36	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 36	
tccatgggggt tggtaggaac	20
<210> 37	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 37	
ggtgacagag taaaactatc tg	22
<210> 38	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 38	
gacccccagt agacgttgt	20
<210> 39	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 39	
gtaaaaaaatc atgagccctg c	21
<210> 40	
<211> 20	
<212> DNA	

<213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide

<400> 40
 ccagagttag tgaggcggtc

20

<210> 41
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 41
 gaagcgtaa ggacccac

20

<210> 42
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 42
 atctatctt ccaatttcc ac

22

<210> 43
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 43
 gtcctgttaa acaaagtgc g

21

<210> 44
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 44
 tggggttact ctatgttgt c

21

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

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<400> 45
ctagcacagt atgccctaag 20

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 46
tgaggaaatgt gctgagggtc 20

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 47
gctgtctcct accccatctg 20

<210> 48
<211> 283
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 1

<221> misc_feature
<222> (1)...(283)
<223> n = A,T,C or G

<400> 48
gtaggctggg gcgggggctg gaggctgggg ctggggctgg ggctggcgta tggcaactagg 60
gctgaactag gaccaggcca tggagaatgg aggatggagg ccggggatgc gcaccaggc 120
cgggcttagga ctagggtctgg agcggggcct gggggctggg gctgggcgtt ggcacttaggg 180
cggttgggg ctggggctgg ggctggggga tggagcgggg ccggggctg ggggtggggc 240
tggggatcg actagggtctg gnttaggacc aggcggttgg cat 283

<210> 49
<211> 375
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 1

<221> misc_feature
<222> (1)...(375)
<223> n = A,T,C or G

<400> 49
ggatgggttggg tggaggctgg gggatggcag tagggccggg ctaggactgg ggctggagcg 60
gagtttgggg ctggggctca ggagcggggg ctggggctgg ggctggggct gggggatggc 120
actagggttggg gggcacatc ccaggaggc cggtggggc agagctgagt 180

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ccgcggggc cggaccccg aagccaagcn gccggcctgc aggatgaggc ctggctcc 240
 ggcctatgacc acagacgtgc cagacttaag tacggagacc tgaggagcca ggctgcagtt 300
 ggcctacttt ncnctaagct ggggtggac cagtggtaac ctccctccgaa gtgggttctg 360
 ctcttcttag cctag 375

<210> 50
 <211> 439
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 1

<221> misc_feature
 <222> (1)...(439)
 <223> n = A,T,C or G

<400> 50
 ccactgccac tgccaccagt ttgcacccct aacccctgtn ctgctcctcc caccccaagg 60
 cagagccgn gaaagggaaac agtttgtcc ctccctggtc gctgcggaag agtctcacca 120
 tcctctgtc tccgtagcta gaaaggaggc agaacccaca ttccggaggga ggttaccact 180
 ggtccacccc cagcttagcg caaatggc caacctgcatt gcctggnnct cctcaggntc 240
 tgcctactta agtctggcag ctctnnntca tggccgaggt agccaggctc atcctgcagg 300
 nnccngccnn ttgncttncc ggggntcgn nncccccgtac tcagctcgtc cagccggct 360
 ctggatgtga cctaccgctg ctatgcata ccagccagcc agccagccgt ctagccagcc 420
 aactgctcag ccagtcttag 439

<210> 51
 <211> 368
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 1

<221> misc_feature
 <222> (1)...(368)
 <223> n = A,T,C or G

<400> 51
 caaaggccat caggagtggg gaagaacac ggcaaaatgt agccacattt acagccata 60
 aganagccag caaagccgtc tagcctccaa gcacccctgcg aaacctcaag tactgcggtc 120
 tggtaagctc ctggcccaga ggggacggcg gtccaggng ccctccctt gctggctctg 180
 cctattctaa agccctggcc cgnctccttc ccgaaaagcc ccttggtgcc actgccactg 240
 ccaccanttt gcnccccata ccctgtntc ctcctccccac cccaaaggcag atgcggnnng 300
 ngaaaggaaa cantttggc ctcctggc ggctcgngga agactcctca ccatccttcc 360
 tgtcttcc 368

<210> 52
 <211> 400
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 2

<400> 52
 gaatattttac gagggtggc tgaacagtga ctatgtccac ctgtttgtgg ccacattgt 60
 ctttccacat gttccaaaca tcacccgtta caaggcaagg atgaaatgtt ggaatccctt 120
 cctggatgtc atcggtttt gggctctttt gttgtggat gagatttggg agttctatgt 180

tgaaatgagt gagcccgaa aacggttcat gtctcagttc cccttgaaa ggtgtagaag 240
 ttaagagttt gagatgcgtg gagcagttaa taccatcaa gctttgtgt gggttctgaa 300
 aatcggtcca gtgagtagt agggcatgg gatTTtagag gtggacatga tcaaattccat 360
 ctttagagatc aacacatctc actcattttt attttcttat 400

<210> 53
<211> 418
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 2

<221> misc_feature
<222> (1)...(418)
<223> n = A,T,C or G

<400> 53
tttgaggta gacaggactg ggttcaggc ccagctctgc cacatatagt cttggcaag 60
tggagtaagc gctctctgtc cctcagttcc ctcatctgtaa aatgagaac gatagtgc 120
actccatggg gttggtagga acaaagaaga ttttggcat gtaaagttct tagtgc 180
tgcacagtgg tctgttaagt aagctgcgtt tcttagtggta agaaggagct gattgatggc 240
cctggctgag aactttgtt tcgcTTTTC ccTTTTAAT tcaggatcag ttacagttgt 300
ggattcgagg caacgtgaat gcctgtgcga ggtccatctt catattgtat gaaatggata 360
agatgcatgc aggccata gatgcntca anccttcctt cgactattat gacctggt 418

<210> 54
<211> 198
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 3

<400> 54
ctcgactatt atgacacctt ggtatgggtc tcctaccaga aagccatgtt catatttctc 60
aggtaaggc agggcttaga catgtatggat gggccccgag cccaaGCCTC tgagctccag 120
gagaaaaccc tgccttacc cactggatt gtttgcagc aatgctggag cagaaaggat 180
cacagatgtt tttggatt 198

<210> 55
<211> 536
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 4

<221> misc_feature
<222> (1)...(536)
<223> n = A,T,C or G

<400> 55
gtctgtgtcg gtttcaata acaagaacag gtgagtaggg ccattccaccg ccagtccc 60
ctgggtccta atcctgcacc ctaagtgtt aaagcatcag ggtcaactgtc agcatcacct 120
gggagctggg tagaaagaaa tggagattct cagtccctt ccgagtcgtg agggaaatct 180
ttgctgtatgtt actccaggtt acttttatgtt acactaatgtt ttgacaagtgtt ctgttttattt 240
tttatttttcc agatagttt actctgtcac ctggctgaa gtgcgtggc gtaaccttgc 300
ctcaactgcaaa cctctgcctc ccgggctcaa gcgattcttgc tgcctcagcc tcctgagtag 360
ctgggatttttcc aggtgcacac catgcccaag cnaatattttt gtatTTtag tagaganggg 420

gccccgtnc a tgttaaccag gctggcttg aactnttacc tcaggtgagt ccnccacac 480
 ggcctccaa agtgctggg ttacaggcgt gagccactgt gtctcagctt attttt 536

<210> 56
 <211> 1302
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 4

<221> misc_feature
 <222> (1)...(1302)
 <223> n= A,T,C or G; m= A,or C; r= G,or A; w= A,or T; y= C,or T

<400> 56

gccactccaa gctaccatct gagattgttt cctgccctag agtgttaaag gcgtgaggc 60
 cgtctgccct cagctgtgtc cccaggccca gggcgtgcct ggcaacanna gcaggcctct 120
 gagaaccagc ctcccacgtg agttcatgtat agnaagacag cccctcggtc ccattcagtg 180
 gttggttctg ttcttlycct ggcmtataagc tccactctgy mrtcagccam acatttattt 240
 agtaccagtt gttggcaaag cactgttggg catgaaaagc attaaccagg tgaatgagga 300
 ggagcttggg ttgggacgga gcmcaraaw tacatggcag accagaagga aatcagctca 360
 agtagaaara cacgcatggg ctcgtggcgc acgcagtgt tgctgtgtca tctggggctg 420
 ggagaagtg tcctggatca ggagttccag gagcccagga ggagtggacg ggtcagtgc 480
 gagccagccc gcaatcaggg gaagaaaaca cggccaaggc caggccttca cggggagccc 540
 agcgtggct gcacatctgc actctccagg ctatgttgg tgcccacatg ctctgcagg 600
 tctgggact gtggcaggg cagcaggctt ccctgttgc agtccagctg ctgaaaactcc 660
 agggagagtc aaaaagttcc caaatacaga ggcgtggctg gtatgccttc cgggaaattc 720
 ttcttgcttc ccgccttctg tggactctg cttcccccac tctgcctctc tgcttggatc 780
 tggggcccaag gaccttttc ccatcttca tctcttaagt cataccttgg gaggcctccc 840
 ccagcccccc gtgtaaagag ggctgtcaca gcttctgtc tcacagaagc attacaatgt 900
 gcaggtgcct gttAACATCT gcctccca ctatcttgc gctccacaag ggagagggca 960
 cacccttagt gtatgtgtgg gatggatagg aggggtggatg acacccagta gatgtgtatg 1020
 ggtatggatag gagggtggat gacacccagt aggtgtgtat gggatggatg ggagggtggg 1080
 tgacccttag tagatgtggg ggggtgggt ggggtacccc cagtaggtgt gtgtggatc 1140
 gatagggtgac ccccagtata cggttgggg acggatgggaa ggttaggtaa gtgaccccca 1200
 ggaggcgtct atagggcagg tgggtggatg tggatgaaca gcacattgtt tcttcttccc 1260
 aggtggcttc tggcacagca gcttaattga ccggAACCTC at 1302

<210> 57
 <211> 240
 <212> DNA
 <213> Unknown

<220>
 <223> TORB intron 1-5'

<221> misc_feature
 <222> (1)...(240)
 <223> n = A,T,C or G

<400> 57

ggagcggccg ctcaacgcctt cgggtacggc ggcgcgcga gctgtgggtc ggcgcgtgcgg 60
 ggggcgcggg ggcgcggggg cgcggaggaa cggcctcggt ggcgcctggc acggaccggg 120
 cccgtggcat cttagacggcg gtgggtccag ctgggtggg cggggagcgg atggggcggc 180
 cccggaaccgg ttcgcnggaa cgcagaagcn gtgccttgcgaa acactctcag atcgtgnccc 240

<210> 58
 <211> 310

<212> DNA
<213> Unknown

<220>
<223> TORB intron 1-3'

<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

<400> 58
gggaccaaag gacgtccgtc gttcccaccc accctaatacg ttgcgcngtc ngttcgctac 60
ccagtagaga gacttactta cnngtnnate gaaggaatag tctgggcctt cgcaattcct 120
ggaggtgtat tagaacttcc accgttagcaa actgacggag ccggatccc acaccgcctg 180
tgggnncgac acgggaccta ttgacacgaa gaacgaaacn gtcgattctt tcacgacgca 240
acgactacgt aaaaattcca gacaaagaga gaaacaagac cccgacaaga acgtcgagag 300
ttcgacctaa 310

<210> 59
<211> 401
<212> DNA
<213> Unknown

<220>
<223> TORB intron 2-5'

<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 59
caggaacaac aaaaatccca agaaaacctt gaccctttcc ttacacggct gggctggcac 60
aggcaagaat tttgtcagtn aaattgtggc tgaaaatctt cacccaaaag gtctgaagag 120
taactttgtc cacctgtttg tatcgactct gcacttcctt catgagcaga agataaaaact 180
gtaccaggca agagaacccg ctattatctc gtctgcaggc cagtcggact ggtccgggtg 240
acctgctcac taactctggc ctctgcttct ctttcctttg tggctgtta gcccccgct 300
ccactgagtt aaggcacact tagtccaggt agttacaag ctctcctaca acatttctta 360
cttggttcca aaacagtcca gtgggtttagg ggatgttatt t 401

<210> 60
<211> 238
<212> DNA
<213> Unknown

<220>
<223> TORB intron 2-3'

<400> 60
ttctgtaact ggtcctggac caaccatgaa agaagaaaaca ggatgcgaag ctcaaaggcc 60
tgcaccaaga ggcgcgcagg ctccatctgc tcctcatgca ctgaaggacg aggtcagagc 120
tcttagaatg gcaccctcac ccccactcgc taggttagcag cttttctaaa accttatctc 180
taaaaaagtgg aaattggcag agatagatgc taaaatgcag agaagttttt cctaactc 238

<210> 61
<211> 391
<212> DNA
<213> Unknown

<220>
<223> TORB intron 3-5'

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<221> misc_feature
<222> (1)...(391)
<223> n = A,T,C or G

<400> 61
gggatcattg acgcaatcaa gccgttctta gactactacg agcaggttga cggagtgtct 60
taccgcaaag ccatcttcat ctttctcagg tcagcggag gcggtttttt ggggcacaca 120
agcccttcatt tctctcaatg ataaaatgag gtcctgagga ccatcagcac tttgtttacc 180
aggacgaaag tgcctgcttg gcacaaggca cttacctact gctttacttt tcctttgccta 240
gtcattcagca tggcacacag tgtgggttgt ggaaatgaac taaagaaaata atcaactggga 300
caggcgcgggt ggctcacacc tgtaatccn agcactttgg gnaggcatgg cgggcggatc 360
acaggagatc gagacatctg ctaacatgnt g 391

<210> 62
<211> 373
<212> DNA
<213> Unknown

<220>
<223> TORB intron 3-3'

<221> misc_feature
<222> (1)...(373)
<223> n = A,T,C or G

<400> 62
gtaagacaca gagtctttt tnttttttag accgagtnnc attnttggttt ccnangctgg 60
agtgaatgg catgatctcg gctcgctgca acctccacctt cccgrrttca aacgattctc 120
ccacccatcgcc ctccccatgtt gctgggatta cagncatgca ccaccattag cctggctaat 180
ttttgtgttt ttagtagaga tggggttact ctatgttggt caggctggcc ttgaactccc 240
gacctcaggt gatctacccg cctccggctc ccaaagtgtt gggattacag ccatgagcna 300
ccacnscnan cagacncaga agtcttaata tgtgattttt atctttatcc ctctggcaaa 360
ctcagcaatg cag 373

<210> 63
<211> 310
<212> DNA
<213> Unknown

<220>
<223> TORB intron 4'

<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

<400> 63
gtgagtcac caggtaaag gagccctta actgtccacg agtgagccgt ctgcttttc 60
attgagtgtt tgcacaaagc cacaggatcc cactggattt cctcaactttt ctaaagtca 120
gaattttctt agggcataact gtgcttagaaa ccagtggatg agtgcacccg tgagtccctcg 180
atgggcttgc tgcacactga caagagacnc tctcaagggg tacggacatg aggaatgtgc 240
tgagggtcgg gactggagct tggccaggtg gcggtgggtgg cagggaaaccc agctgtgtct 300
tgttctgcag 310

<210> 64
<211> 12
<212> DNA
<213> Artificial Sequence

<220>

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<223> Synthetic Oligonucleotide

<400> 64

gaattcctta ag

12

<210> 65

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Peptide

<223> Xaa at position 2, 5 is a variable residue
 Xaa at position 8 is a threonine or a serine
 residue

<221> VARIANT

<222> (1)...(8)

<223> Xaa = Any Amino Acid

<400> 65

Gly Xaa Thr Gly Xaa Gly Lys Xaa
 1 5

<210> 66

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Peptide

<223> Xaa at position 2, 3, 4, 8 is a hydrophobic residue
 Xaa at position 11 is a variable residue

<221> VARIANT

<222> (1)...(12)

<223> Xaa = Any Amino Acid

<400> 66

Ser Xaa Xaa Xaa Phe Asp Glu Xaa Glu Lys Xaa His
 1 5 10

<210> 67

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 67

gtaggctggg

10

<210> 68

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 68
gcaaggatgg 10

<210> 69
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 69
gtaaggtcag 10

<210> 70
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 70
gtgagtaggg 10

<210> 71
<211> 10
<212> DNA
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<220>

<223> Exon/intron of DYT1

<400> 71
tctttccca 10

<210> 72
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 72
tttaattcag 10

<210> 73
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 73

tgttttgcag

10

<210> 74

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 74

ttcttcccag

10

<210> 75

<211> 11

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 75

cactgcagaa g

11

<210> 76

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 76

caatgctgga

10

<210> 77

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of TORB

<400> 77

tggcttctgg

10

<210> 78

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of TORB

<400> 78	
gcaagagaac	10
<210> 79	
<211> 10	
<212> DNA	
<213> Unknown	
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<400> 79	
gtcagcggga	10
<210> 80	
<211> 10	
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<400> 80	
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<210> 81	
<211> 10	
<212> DNA	
<213> Unknown	
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<400> 81	
gttcttgcag	10
<210> 82	
<211> 10	
<212> DNA	
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<400> 82	
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<210> 83	
<211> 10	
<212> DNA	
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gcaaactcag	10
<210> 84	
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<212> DNA
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<220>
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<400> 84
 tgttctgag

9

<210> 85
 <211> 11
 <212> DNA
 <213> Unknown

<220>
 <223> Exon/intron of TORB

<400> 85
 ctctcaagct g

11

<210> 86
 <211> 10
 <212> DNA
 <213> Unknown

<220>
 <223> Exon/intron of TORB

<400> 86
 caatgcaggc

10

<210> 87
 <211> 10
 <212> DNA
 <213> Unknown

<220>
 <223> Exon/intron of TORB

<400> 87
 tggcctgtgg

10

<210> 88
 <211> 378
 <212> DNA
 <213> Unknown

<220>
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<221> misc_feature
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<400> 88
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 acagccccata aganagccag caaagccgtc tagcctccaa gcacccgtcg aaacccctcaag 120
 tactgcggtc tggtaagctc ctggcccaga ggggacggcg gtccagggnng ccctcccttt 180
 gctggtcctg cctattctaa agccctggcc cgnctcccttc ccgaaaagcc ccttggtgcc 240

actgccactg ccaccanttt gcnccccctac ccctgtncgt ctccctccac cccaaggcag 300
atgcggnnng nngaaggaaa cantttggtc cctcctggtc ggctcgngga agactcctca 360
ccatccttcc tgtcttcc 378

<210> 89
<211> 402
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 2

<400> 89
gaatattttac gagggtggtc tgaacagtga ctatgtccac ctgtttgtgg ccacattgct 60
ctttccacat gcttcaaaca tcaccttgc taaggcaagg atggaagttt ggaatccctt 120
cctggatgtc atcgggtttt gggctcttt gttgtggat gagatttggg agttctatgt 180
tgaatagt gagccccgaa aacggttcat gtctcagttc cccttggaaa ggtttagaaag 240
ttaagagttt gagatgcgtg gagcagttaa taccatcaa gctttgtggt gggttctgaa 300
aatcggtcca gtgagttatgt agggtcatgg gatttttagag gtggacatga tcaaattccat 360
cttagagatc aacacatctc actcattttt attttcttat tt 402

<210> 90
<211> 200
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 3

<400> 90
ctcgactatt atgacctggc ggttgggtc tccttaccaga aagccatgtt catatttctc 60
aggtaaggc agggcttagga catgtatggat gggccccgag cccaaaggctc tgagctccag 120
gagaaaaccc tgccttacc cactggatt gttttgcagc aatgtggag cagaaaaggat 180
cacagatgtg gctttggatt 200